

Shears, Beverly

From: Devi, Sarvamangala
Sent: Monday, June 10, 2002 7:17 AM
To: Shears, Beverly
Subject: 09/388,090

Good morning Beverly:

Would you please perform a text search for the following claim:

An isolated nucleic acid (DNA) comprising a nucleotide sequence encoding a polypeptide of a *Neisseria* species, which polypeptide has a molecular weight of about 40 kD to about 55 kD and contains a serine protease motif.

Note: Examples of *Neisseria* species include *Neisseria gonorrhoea* (gonococcus); *Neisseria catarrhalis*; *Neisseria lactamica*; *Neisseria ovis*; *Neisseria lacunata*; *Neisseria bovis*; and *Neisseria osloensis*.

Please cover all databases, especially Medical, veterinary and agricultural databases; Dissertation Abstracts; Inside Conferences; PASCAL; JICST.

Thank you.

S. DEVI, Ph.D.
AU 1645
CM1-7E15
Mailbox: 7E12

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

Dev, S.
09/388090

09/388090

17jun02 10:11:49 User219783 Session D1832.1

SYSTEM:OS - ~~09/388090~~

File 35:Dissertation Abs Online 1861-2002/May
(c) 2002 ProQuest Info&Learning
File 65:Inside Conferences 1993-2002/Jun W2
(c) 2002 BLDSC all rts. reserv.
File 77:Conference Papers Index 1973-2002/May
(c) 2002 Cambridge Sci Abs
File 144:Pascal 1973-2002/Jun W3
(c) 2002 INIST/CNRS
File 266:FEDRIP 2002/Apr
Comp & dist by NTIS, Intl Copyright All Rights Res
File 440:Current Contents Search(R) 1990-2002/Jun 17
(c) 2002 Inst for Sci Info
File 348:EUROPEAN PATENTS 1978-2002/Jun W02
(c) 2002 European Patent Office
File 357:Derwent Biotech Res. 1982-2002/Mar W5
(c) 2002 Thomson Derwent & ISI
*File 357: Price changes as of 1/1/02. Please see HELP RATES 357.
Derwent announces file enhancements. Please see HELP NEWS 357.
File 113:European R&D Database 1997
(c)1997 Reed-Elsevier(UK)Ltd All rts reserv
*File 113: This file is closed (no updates)

Set Items Description
--- ----

Set	Items	Description
S1	131177	(NUCLEIC OR DEOXYRIBONUCLEIC OR DEOXY(W)RIBONUCLEIC OR DNA) AND NUCLEOTIDE? ?
S2	73131	S1 AND (POLYPROTEIN? ? OR POLYPEPTIDE? ? OR PROTEIN? ? OR - PEPTIDE? ?)
S3	804	S2 AND (NEISSER? OR (NEISSER? OR N) (W) (GONOCOCC? OR GONORR- H? OR CATARRHAL? OR LACTAMIC? OR OVIS OR LACUNATA OR BOVIS OR
S17	309	MOTIF? ?(S) ((SERINE OR SER) (W) (PROTEASE? ? OR PROTEINASE? - ?))
S18	1	S3 AND S17

>>>No matching display code(s) found in file(s): 65, 113

Key terms
w/ term
ser protease

18/3,AB/1 (Item 1 from file: 348)
DIALOG(R)File 348:EUROPEAN PATENTS
(c) 2002 European Patent Office. All rts. reserv.

01270274
Lawsonia intracellularis proteins, and related methods and materials
Lawsonia intracellularis Proteine sowie Methoden und Materialien die diese verwenden
Proteines de Lawsonia intracellularis et procedes et materiaux relatifs a ces proteines
PATENT ASSIGNEE:
Pfizer Products Inc., (2434221), Eastern Point Road, Groton, Connecticut 06340, (US), (Applicant designated States: all)
INVENTOR:
Rosey, Everett Lee, Pfizer Central Research, Eastern Point Road, Groton, Connecticut 06340, (US)
LEGAL REPRESENTATIVE:

Searcher : Shears 308-4994

09/388090

Eddowes, Simon et al (87482), Urquhart-Dykes & Lord, 30 Welbeck Street,
London W1G 8ER, (GB)
PATENT (CC, No, Kind, Date): EP 1094070 A2 010425 (Basic)
EP 1094070 A3 020109
APPLICATION (CC, No, Date): EP 2000309125 001017;
PRIORITY (CC, No, Date): US 160922 P 991022
DESIGNATED STATES: AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LI;
LU; MC; NL; PT; SE
EXTENDED DESIGNATED STATES: AL; LT; LV; MK; RO; SI
INTERNATIONAL PATENT CLASS: C07K-014/205; C12N-015/31

ABSTRACT EP 1094070 A2

Isolated polynucleotide molecules contain a nucleotide sequence that encodes a L. intracellularis HtrA, PonA, HypC, LysS, YcfW, ABC1, or Omp100 protein, a substantial portion of the sequences, or a homologous sequence. Related polypeptides, immunogenic compositions and assays are described.

ABSTRACT WORD COUNT: 40

NOTE:

Figure number on first page: 1

LANGUAGE (Publication,Procedural,Application): English; English; English
FULLTEXT AVAILABILITY:

Available Text	Language	Update	Word Count
CLAIMS A	(English)	200117	864
SPEC A	(English)	200117	25111
Total word count - document A			25975
Total word count - document B			0
Total word count - documents A + B			25975

Set	Items	Description
S4	71439	(NUCLEIC OR DEOXYRIBONUCLEIC OR DEOXY(W)RIBONUCLEIC OR DNA-) (S)NUCLEOTIDE? ?
S5	32164	S4(S) (POLYPROTEIN? ? OR POLYPEPTIDE? ? OR PROTEIN? ? OR PE- PTIDE? ?)
S6	124	S5(S) (NEISSER? OR (NEISSER? OR N) (W) (GONOCOCC? OR GONORRH? OR CATARRHAL? OR LACTAMIC? OR OVIS OR LACUNATA OR BOVIS OR OS- LOENSIS))

S8 69 S6(S)ENCOD?

S10 17 S8(S) (ISOLAT? OR ISOL? ?)

S19 17 S10 NOT S18

>>>No matching display code(s) found in file(s): 65, 113

19/3,AB/1 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal
(c) 2002 INIST/CNRS. All rts. reserv.

11092874 PASCAL No.: 93-0599895
Cloning and characterization of Neisseria meningitidis genes encoding the transferrin-binding proteins Tbp1 and Tbp2
LEGRAIN M; MAZARIN V; IRWIN S W; BOUCHON B; QUENTIN-MILLET M J; JACOBS E; SCHRYVERS A B
Transgene, 67082 Strasbourg, France; Pasteur-Merieux serums vaccins,
69280 Marcy L'Etoile, France
Journal: Gene, 1993, 130 (1) 73-80

w/o term
Ser protease

Searcher : Shears 308-4994

Language: English

Genes *tbp1* and *tbp2*, *encoding*** the transferrin-binding *proteins***
Tbp1 and *Tbp2*, have been *isolated*** from two strains of *Neisseria***
 meningitidis. The *tbp2* and *tbp1* open reading frames are tandemly arranged
 in the genome with an 87-bp intergenic region, and the *DNA*** region
 upstream from the *tbp2*-coding sequence contains domains homologous to
Escherichia coli promoter consensus motives. *Nucleotide*** sequence
 analysis suggests the existence of a *Tbp1* precursor carrying an N-terminal
 signal *peptide*** with a peptidase I cleavage site and of a *Tbp2* precursor
 with N-terminal homology to lipoproteins, including a peptidase II cleavage
 site. Comparison of the *Tbp1* deduced amino acid (aa) sequences from both
 strains showed about 76% aa homology, while those of *Tbp2* revealed only
 about 47% aa homology

19/3,AB/2 (Item 1 from file: 440)
 DIALOG(R)File 440:Current Contents Search(R)
 (c) 2002 Inst for Sci Info. All rts. reserv.

12441791 References: 41

TITLE: *exl*, an exchangeable genetic island in *Neisseria meningitidis*
 AUTHOR(S): Kahler CM (REPRINT); Blum E; Miller YK; Ryan D; Popovic T;

Stephens DS

AUTHOR(S) E-MAIL: charlene.kakler@monash.edu.au

CORPORATE SOURCE: Monash Univ, Dept Microbiol, Wellington Rd/Clayton/Vic
 3800/Australia/ (REPRINT); Emory Univ, Dept Med, /Atlanta//GA//; Emory
 Univ, Dept Microbiol & Immunol, /Atlanta//GA/30322; Vet Adm Med Ctr, Res
 Serv, /Atlanta//GA/30033; Ctr Dis Control & Prevent, /Atlanta//GA//; State
 Univ W Georgia, /Carrollton//GA/

PUBLICATION TYPE: JOURNAL

PUBLICATION: INFECTION AND IMMUNITY, 2001, V69, N3 (MAR), P1687-1696

GENUINE ARTICLE#: 404GZ

PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904
 USA

ISSN: 0019-9567

LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: The genetic structure and evolution of a novel exchangeable
 meningococcal genomic island was defined for the important human pathogen
 *Neisseria*** meningitidis, In 125 meningococcal strains tested, one of
 three unrelated *nucleotide*** sequences, designated *exl* (exchangeable
 locus), was found between a gene required for heme utilization, *hemO*, and
col, *encoding*** a putative *Escherichia coli* collagenase homologue. The 5'
 boundary of each *exl* cassette was the stop codon of *hemO*, whereas the 3'
 boundary was delineated by a 33-bp repeat containing *neisserial*** uptake
 sequences located downstream of *col*. One of the three alternative *exl*
 cassettes contained the meningococcal hemoglobin receptor gene, *hmbR*
 (*exl3*), In other meningococcal strains, *hmbR* was absent from the genome and
 was replaced by either a *nucleotide*** sequence containing a novel open
 reading frame, *exl2*, or a cassette containing *exl3*. The *proteins***
 *encoded*** by *exl2* and *exl3* had no significant amino acid homology to *HmbR*
 but contained six motifs that are also present in the lipoprotein
 components of the lactoferrin (*LbpB*), transferrin (*TbpB*), and
 hemoglobin-haptoglobin (*HpuA*) uptake systems. To determine the evolutionary
 relationships among meningococci carrying *hmbR*, *exl2*, or *exl3*, *isolates***
 representing 92 electrophoretic types were examined. *hmbR* was found
 throughout the population structure of *N. meningitidis* (genetic distance,
 >0.425), whereas *exl2* and *exl3* were found in clonal groups at genetic

09/388090

distances of <0.2. The commensal *neisserial*** species were identified as reservoirs for all of the exl cassettes found in meningococci. The structure of these cassettes and their correlation with clonal groups emphasize the extensive gene pool and frequent horizontal *DNA*** transfer events that contribute to the evolution and virulence of *N. meningitidis*.

19/3,AB/3 (Item 2 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)
(c) 2002 Inst for Sci Info. All rts. reserv.

08050730 References: 16
TITLE: Molecular cloning and expression of NlaIII restriction-modification system in E-coli
AUTHOR(S): Morgan RD; Camp RR; Wilson GG; Xu SY (REPRINT)
CORPORATE SOURCE: NEW ENGLAND BIOLABS INC, 32 TOZER RD/BEVERLY//MA/01915 (REPRINT); NEW ENGLAND BIOLABS INC, /BEVERLY//MA/01915; GORDON COLL, DEPT BIOL/WENHAM//MA/01984
PUBLICATION TYPE: JOURNAL
PUBLICATION: GENE, 1996, V183, N1-2 (DEC 12), P215-218
GENUINE ARTICLE#: VZ989
PUBLISHER: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS
ISSN: 0378-1119
LANGUAGE: English DOCUMENT TYPE: ARTICLE

ABSTRACT: The NlaIII restriction enzyme *isolated*** from *Neisseria*** *lactamica*** recognizes the sequence 5'-CATG-3', cleaving after the G to generate a four base 3' overhang. The NlaIII methylase and a portion of the NlaIII endonuclease gene were cloned into *E. coli* by the methylase selection method, and the remaining portion of the NlaIII endonuclease gene was cloned by inverse PCR. The *nucleotide*** sequence of the endonuclease gene and the methylase gene were determined. The NlaIII endonuclease gene is 693 bp, *encoding*** a *protein*** with predicted molecular weight of 26 487. The NlaIII methylase gene was identical with that previously reported [Labbe, D., Joltke, H.J. and Lau, P.C. (1990) Cloning and characterization of two tandemly arranged *DNA*** methyltransferase genes of *Neisseria*** *lactamica***: an adenine-specific M.NlaIII and a cytosine-type methylase. *Mol. Gen. Genet.* 224, 101-110]. The endonuclease and methylase genes overlap by four bases and are transcribed in the same orientation. The endonuclease gene was cloned into an improved T7 vector, and a high level of NlaIII endonuclease expression was achieved in *E. coli*.

19/3,AB/4 (Item 3 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)
(c) 2002 Inst for Sci Info. All rts. reserv.

07535767 References: 45
TITLE: ANTIGENIC DIVERSITY OF MENINGOCOCCAL OUTER MEMBRANE PROTEIN PORIN HAS IMPLICATIONS FOR EPIDEMIOLOGICAL ANALYSIS AND VACCINE DESIGN
AUTHOR(S): FEATHERS IM; FOX AJ; GRAY S; JONES DM; MAIDEN MCJ (Reprint)
CORPORATE SOURCE: NATL INST BIOL STAND & CONTROLS, DIV BACTERIOL, BLANCHE LANE S MIMMS/POTTERS BAR EN6 3QG/HERTS/ENGLAND/ (Reprint); NATL INST BIOL STAND & CONTROLS, DIV BACTERIOL/POTTERS BAR EN6 3QG/HERTS/ENGLAND/; WITHINGTON HOSP, MRU PUBL HLTH LAB/MANCHESTER M20 8LR/LANCS/ENGLAND/
PUBLICATION: CLINICAL AND DIAGNOSTIC LABORATORY IMMUNOLOGY, 1996, V3, N4 (JUL), P444-450
GENUINE ARTICLE#: UV503

ISSN: 1071-412X

LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: The currently used serological subtyping scheme for the pathogen *Neisseria meningitidis* is not comprehensive, a proportion of *isolates* are reported as not subtypeable (NST), and few *isolates* are fully characterized with two subtypes for each strain. To establish the reasons for this and to assess the effectiveness of *DNA*-based subtyping schemes, dot blot hybridization and *nucleotide* sequence analyses were used to characterize the genes *encoding* antigenic variants of the meningococcal subtyping antigen, the PorA *protein*. A total of 233 strains, including 174 serologically NST and 59 partially or completely subtyped meningococcal strains, were surveyed. The NST *isolates* were chosen to be temporally and geographically representative of NST strains, *isolated* in England and Wales, and submitted to the Meningococcal Reference Unit in the period 1989 to 1991. The *DNA*-based analyses demonstrated that all of the strains examined possessed a *porA* gene. Some of these strains were serologically NST because of a lack of monoclonal antibodies against certain PorA epitopes; in other cases, strains expressed minor variants of known PorA epitopes that did not react with monoclonal antibodies in serological assays. Lack of expression remained a possible explanation for serological typing failure in some cases. These findings have important implications for epidemiological analysis and vaccine design and demonstrate the need for genetic characterization, rather than phenotypic characterization using monoclonal antibodies, for the identification of meningococcal strains.

19/3,AB/5 (Item 4 from file: 440)
 DIALOG(R)File 440:Current Contents Search(R)
 (c) 2002 Inst for Sci Info. All rts. reserv.

06475536 References: 56

TITLE: CHARACTERIZATION OF THE PILF-PILD PILUS-ASSEMBLY LOCUS OF NEISSERIA GONORRHOEAE

AUTHOR(S): FREITAG NE; SEIFERT HS; KOOMEY M (Reprint)

CORPORATE SOURCE: UNIV MICHIGAN, SCH MED, DEPT MICROBIOL & IMMUNOL/ANN ARBOR//MI/48109 (Reprint); UNIV MICHIGAN, SCH MED, DEPT MICROBIOL & IMMUNOL/ANN ARBOR//MI/48109; NORTHWESTERN UNIV, SCH MED, DEPT MICROBIOL IMMUNOL/CHICAGO//IL/60611

PUBLICATION: MOLECULAR MICROBIOLOGY, 1995, V16, N3 (MAY), P575-586

GENUINE ARTICLE#: RC361

ISSN: 0950-382X

LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: Expression of Type IV pilin by the bacterial pathogen *Neisseria gonorrhoeae* appears to be essential for colonization of the human host. Several *N. gonorrhoeae* gene products have been recently identified which bear homology to *proteins* involved in pilus assembly and *protein* export in other bacterial systems. We report here the *isolation* and characterization of transposon insertion mutants in *N. gonorrhoeae* whose phenotypes indicate that the *N. gonorrhoeae pilF* and *pilD* gene products are required for gonococcal pilus biogenesis. Mutants lacking the *pilD* gene product, a pre-pilin peptidase, were unable to process the pre-pilin subunit into pilin and thus were nonpilated, *pilF* mutants processed pilin but did not assemble the mature subunit. Both classes of mutants released S-pilin, a soluble, truncated form of the pilin subunit previously correlated with defects in pilus assembly. In addition,

mutants containing transposon insertions in pild or in a downstream gene, orfX, exhibited a severely restricted growth phenotype. Deletion analysis of pild indicated that the poor growth phenotype observed for the pild transposon mutants was a result of polar effects of the insertions on orfX expression, orfX *encodes*** a predicted *polypeptide*** of 23 kDa which contains a consensus *nucleotide***-binding domain and has apparent homologues in Pseudomonas aeruginosa, Pseudomonas putida, Thermus thermophilus, and the eukaryote Caenorhabditis elegans. Although expression of orfX and pild appears to be transcriptionally coupled, mutants containing transposon insertions in orfX expressed pild. Unlike either pild or pild mutants, orfX mutants were also competent for *DNA*** transformation.

19/3,AB/6 (Item 5 from file: 440)
 DIALOG(R)File 440:Current Contents Search(R)
 (c) 2002 Inst for Sci Info. All rts. reserv.

05954189 References: 32
 TITLE: LIPOOLIGOSACCHARIDE BIOSYNTHESIS IN NEISSERIA GONORRHOEA - CLONING, IDENTIFICATION AND CHARACTERIZATION OF THE ALPHA-1,5 HEPTOSYLTRANSFERASE I GENE (RFAC)
 AUTHOR(S): ZHOU DG; LEE NG; APICELLA MA (Reprint)
 CORPORATE SOURCE: UNIV IOWA, DEPT MICROBIOL, 51 NEWTON RD/IOWA CITY//IA/52242 (Reprint); UNIV IOWA, DEPT MICROBIOL/IOWA CITY//IA/52242
 PUBLICATION: MOLECULAR MICROBIOLOGY, 1994, V14, N4 (NOV), P609-618
 GENUINE ARTICLE#: PU230
 ISSN: 0950-382X
 LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: The identical partial deep-core structure of Hep alpha 1-3Hep alpha 1-5KDO in Salmonella typhimurium LT2 LPS and *Neisseria*** *gonorrhoeae*** LOS enabled us to *isolate*** a *DNA*** fragment from *N*** . *gonorrhoeae*** that was able to complement the alpha 1,5 LOS heptosyltransferase defect in the S. typhimurium rfaC630 (SA1377) mutant. SDS-PAGE analysis confirmed the production of wild-type LPS in the transformant. Subcloning revealed that complementation was due to a 1.2 kb fragment. Sequence analysis revealed a complete open reading frame capable of *encoding*** a 36-37 kDa *peptide***. In vitro transcription-translation analysis of the 1.2 kb clone confirmed that a 37 kDa *protein*** was *encoded*** by this *DNA*** fragment. The *DNA*** sequence-deduced *protein*** had 36% identity and 58% similarity to S. typhimurium heptosyltransferase (RfaC). Primer extension analysis indicated that transcription of the cloned gene in *N***. *gonorrhoeae*** strain 1291 begins 144 bp upstream of the start codon at a G *nucleotide***. An isogenic mutant of *N***. *gonorrhoeae*** strain 1291 with an m-Tn3 insertion inside the coding sequence expressed a single truncated LOS with a similar molecular mass to S. typhimurium rfaC LPS. We conclude that the 1.2 kb fragment *encodes*** the alpha 1,5 LOS heptosyltransferase I (RfaC) in *N***. *gonorrhoeae***. Our studies also provide further evidence that the third KDO residue in S. typhimurium LPS is added after the core synthesis is completed.

19/3,AB/7 (Item 6 from file: 440)
 DIALOG(R)File 440:Current Contents Search(R)
 (c) 2002 Inst for Sci Info. All rts. reserv.

05607408 References: 51

TITLE: MOLECULAR CLONING AND ANALYSIS OF GENES FOR SIALIC ACID SYNTHESIS IN
NEISSERIA MENINGITIDIS GROUP B AND PURIFICATION OF THE MENINGOCOCCAL
CMP-NEUNAC SYNTHETASE ENZYME

AUTHOR(S): GANGULI S; ZAPATA G; WALLIS T; REID C; BOULNOIS G; VANN WF;
ROBERTS IS (Reprint)

CORPORATE SOURCE: UNIV LEICESTER, DEPT MICROBIOL/LEICESTER LE1 7RH//ENGLAND/
(Reprint); UNIV LEICESTER, DEPT MICROBIOL/LEICESTER LE1 7RH//ENGLAND//; US
FDA, CTR BIOL EVALUAT & RES, BACTERIAL POLYSACCHARIDES
LAB/BETHESDA//MD/20892

PUBLICATION: JOURNAL OF BACTERIOLOGY, 1994, V176, N15 (AUG), P4583-4589

GENUINE ARTICLE#: NY398

ISSN: 0021-9193

LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: The gene *encoding*** for the CMP-NeuNAc synthetase enzyme of
*Neisseria*** meningitidis group B was cloned by complementation of a
mutant of Escherichia coli defective for this enzyme. The gene (neuA) was
*isolated*** on a 4.1-kb fragment of meningococcal chromosomal *DNA***.
Determination of the *nucleotide*** sequence of this fragment revealed the
presence of three genes, termed neuA, neuB, and neuC, organized in a single
operon. The presence of a truncated ctr A gene at one end of the cloned
*DNA*** and a truncated gene *encoding*** for the meningococcal
sialyltransferase at the other confirmed that the cloned *DNA***
corresponded to region A and part of region C of the meningococcal capsule
gene cluster. The predicted amino acid sequence of the meningococcal NeuA
*protein*** was 57% homologous to that of NeuA, the CMP-NeuNAc synthetase
*encoded*** by E. coli K1. The predicted molecular mass of meningococcal
NeuA *protein*** was 24.8 kDa, which was 6 kDa larger than that formerly
predicted (U. Edwards and M. Frosch, FEMS Microbiol. Lett, 96:161-166,
1992). Purification of the recombinant meningococcal NeuA *protein***
together with determination of the N-terminal amino acid sequence confirmed
that this 24.8-kDa *protein*** was indeed the meningococcal CMP-NeuNAc
synthetase. The predicted amino acid sequences of the two other *encoded***
*proteins*** were homologous to those of the NeuC and NeuB *proteins*** of
E. coli K1, two *proteins*** involved in the synthesis of NeuNAc. These
results indicate that common steps exist in the biosynthesis of NeuNAc in
these two microorganisms.

19/3,AB/8 (Item 7 from file: 440)

DIALOG(R)File 440:Current Contents Search(R)

(c) 2002 Inst for Sci Info. All rts. reserv.

05314950 References: 61

TITLE: ISOLATION AND CHARACTERIZATION OF A GENE INVOLVED IN
HEMAGGLUTINATION BY AN AVIAN PATHOGENIC ESCHERICHIA COLI STRAIN

AUTHOR(S): PROVENCE DL; CURTISS R

CORPORATE SOURCE: ST LOUIS UNIV, SCH MED, DEPT CELL BIOL & PHYSIOL/ST
LOUIS//MO/63110 (Reprint); WASHINGTON UNIV, DEPT BIOL/ST LOUIS//MO/63130

PUBLICATION: INFECTION AND IMMUNITY, 1994, V62, N4 (APR), P1369-1380

GENUINE ARTICLE#: NC074

ISSN: 0019-9567

LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: In this article, we report the *isolation*** and characterization
of a gene that may be important in the adherence of avian pathogenic
Escherichia coli to the avian respiratory tract. The E. coli strain HB101,

which is unable to agglutinate chicken erythrocytes, was transduced with cosmid libraries from the avian pathogenic *E. coli* strain (chi)7122. Enrichment of transductants that could agglutinate thickened erythrocytes yielded 19 colonies. These *isolates*** contained cosmids that encompassed four nonoverlapping regions of the *E. coli* chromosome. Only one group of cosmids, represented by pYA3104, would cause *E. coli* CC118 to agglutinate chicken erythrocytes. A 10-kb fragment of this cosmid was subcloned in pACYC184. Transposon mutagenesis of this fragment, with Tn5seq1 indicated that a contiguous 4.4-kb region of cloned *DNA*** was required for hemagglutination. In vitro transcription/translation assays indicated that this 4.4-kb region of *DNA*** encoded*** one *protein*** of approximately 140 kDa. The *nucleotide*** sequence of this region was determined and found to *encode*** one open reading frame of 4,134 *nucleotides*** that would *encode*** a *protein*** of 1,377 amino acids with a deduced molecular weight of 148,226. This gene confers on *E. coli* K-12 a temperature-sensitive hemagglutination phenotype that is best expressed when cells are grown at 26 degrees C, and we have designated this gene *tsh* and the deduced gene product Tsh. Insertional mutagenesis of the chromosomal *tsh* gene in (chi)7122 had no effect on hemagglutination titers. The deduced *protein*** was found to contain significant homology to the *Haemophilus influenzae* and *Neisseria*** *gonorrhoeae*** immunoglobulin A1 proteases. These data indicate that (i) a single gene *isolated*** from the avian pathogenic *E. coli* strain (chi)7122 will confer on *E. coli* K-12 a hemagglutination-positive phenotype, (ii) (chi)7122 contains at least two distinct mechanisms to allow hemagglutination to occur, and (iii) the hemagglutinin Tsh has homology with a class of *proteins*** previously not known to exist in *E. coli*.

19/3,AB/9 (Item 8 from file: 440)
 DIALOG(R) File 440:Current Contents Search(R)
 (c) 2002 Inst for Sci Info. All rts. reserv.

04797803 References: 36

TITLE: CLONING AND CHARACTERIZATION OF NEISSERIA-MENINGITIDIS GENES
 ENCODING THE TRANSFERRIN-BINDING PROTEINS TBP1 AND TBP2

AUTHOR(S): LEGRAIN M; MAZARIN V; IRWIN SW; BOUCHON B; QUENTINMILLET MJ;
 JACOBS E; SCHRYVERS AB

CORPORATE SOURCE: TRANSGENE SA, 11 RUE MOLSHEIM/F-67082 STRASBOURG//FRANCE/
 (Reprint); UNIV CALGARY, DEPT MICROBIOL & INFECT DIS/CALGARY T2N
 4N1/AB/CANADA/

PUBLICATION: GENE, 1993, V130, N1 (AUG 16), P73-80

GENUINE ARTICLE#: LT636

ISSN: 0378-1119

LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: Genes *tbp1* and *tbp2*, *encoding*** the transferrin-binding *proteins*** *Tbp1* and *Tbp2*, have been *isolated*** from two strains of *Neisseria*** meningitidis. The *tbp2* and *tbp1* open reading frames are tandemly arranged in the genome with an 87-bp intergenic region, and the *DNA*** region upstream from the *tbp2*-coding sequence contains domains homologous to *Escherichia coli* promoter consensus motives. *Nucleotide*** sequence analysis suggests the existence of a *Tbp1* precursor carrying an N-terminal signal *peptide*** with a peptidase I cleavage site and of a *Tbp2* precursor with N-terminal homology to lipoproteins, including a peptidase II cleavage site. Comparison of the *Tbp1* deduced amino acid (aa) sequences from both strains showed about 76% aa homology, while those of *Tbp2* revealed only about 47% aa homology. These comparisons should be

09/388090

extended to other *Neisseria*** strains in order to evaluate further this genetic divergence further.

19/3,AB/10 (Item 9 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)
(c) 2002 Inst for Sci Info. All rts. reserv.

03596664 References: 40

TITLE: SEQUENCE ANALYSIS AND COMPLEMENTATION STUDIES OF THE ARGJ GENE
ENCODING ORNITHINE ACETYLTRANSFERASE FROM NEISSERIA-GONORRHOEAE

AUTHOR(S): MARTIN PR; MULKS MH (Reprint)

CORPORATE SOURCE: MICHIGAN STATE UNIV,DEPT MICROBIOL & PUBL HLTH/E
LANSING//MI/48824 (Reprint); MICHIGAN STATE UNIV,DEPT MICROBIOL & PUBL
HLTH/E LANSING//MI/48824

PUBLICATION: JOURNAL OF BACTERIOLOGY, 1992, V174, N8 (APR), P2694-2701

GENUINE ARTICLE#: HM899

LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: Clinical *isolates*** of *Neisseria*** *gonorrhoeae*** frequently are deficient in arginine biosynthesis. These auxotrophs often have defects in the fifth step of the arginine biosynthetic pathway, the conversion of acetylornithine to ornithine. This reaction is catalyzed by the enzyme ornithine acetyltransferase, which is product of the argJ gene. We have cloned and sequenced the gonococcal argJ gene and found that it contains an open reading frame of 1,218 *nucleotides*** and *encodes*** a *peptide*** with a deduced M(r) of 42,879. This predicted size was supported by minicell analysis. This gene was capable of complementing both Escherichia coli argE and argA mutations and of transforming an ArgJ- strain of *N***. *gonorrhoeae*** to Arg+. Southern blots were able to detect bands that specifically hybridized to the gonococcal argJ gene in genomic *DNA*** from Pseudomonas aeruginosa but not E. coli, a result that reflects the divergent nature of the arginine biosynthetic pathway in these organisms.

19/3,AB/11 (Item 10 from file: 440)
DIALOG(R)File 440:Current Contents Search(R)
(c) 2002 Inst for Sci Info. All rts. reserv.

03474473 References: 33

TITLE: ROLE OF HORIZONTAL GENETIC EXCHANGE IN THE ANTIGENIC VARIATION OF
THE CLASS-1 OUTER MEMBRANE PROTEIN OF NEISSERIA-MENINGITIDIS

AUTHOR(S): FEAVERS IM; HEATH AB; BYGRAVES JA; MAIDEN MCJ

CORPORATE SOURCE: NATL INST BIOL STAND & CONTROLS,DIV BACTERIOL,BLANCHE
LANE/POTTERS BAR EN6 3QG/HERTS/ENGLAND/ (Reprint); NATL INST BIOL STAND &
CONTROLS,DIV INFORMAT/POTTERS BAR EN6 3QG/HERTS/ENGLAND/

PUBLICATION: MOLECULAR MICROBIOLOGY, 1992, V6, N4 (FEB), P489-495

GENUINE ARTICLE#: HE853

LANGUAGE: ENGLISH DOCUMENT TYPE: ARTICLE

ABSTRACT: The *nucleotide*** sequences of the genes *encoding*** the class 1 outer membrane *protein*** of *Neisseria*** meningitidis (PorA) from 15 meningococcal *isolates*** have been examined. These strains, *isolated*** over a number of years, represented a variety of serological types, clonal groups, and geographical locations. Analysis of the aligned *nucleotide*** sequences showed that the known serological relationships between these *proteins*** were not necessarily reflected throughout the *nucleotide***

sequences of their genes. The uneven distribution of base substitutions, revealed by a comparison of the informative bases, suggested that these genes possessed a mosaic structure. This structure probably resulted from the horizontal transfer of *DNA*** between strains and would have contributed to both the generation and the spread of novel antigenic variants of the *protein***. In addition, the *nucleotide*** differences between porA genes from different strains were not consistent with the *nucleotide*** sequence divergence of the whole chromosome, as indicated by pulsed-field gel electrophoresis (PFGE) fingerprinting techniques: some strains with divergent PFGE fingerprints shared porA genes with extensive regions of *nucleotide*** sequence identity and, conversely, some strains with similar chromosome structures possessed porA genes with different *nucleotide*** sequences and serological properties. This suggested that entire genes had been exchanged between strains. Given that the meningococcal class 1 OMP is a major component in novel vaccines, some of which are currently undergoing field trials, the potential of horizontal genetic exchange to generate antigenic diversity has implications for the design of such vaccines.

19/3,AB/12 (Item 1 from file: 357)
 DIALOG(R) File 357:Derwent Biotech Res.
 (c) 2002 Thomson Derwent & ISI. All rts. reserv.

0258656 DBA Accession No.: 2000-13146 PATENT
 Neisseria meningitidis serogroup-B antigen - vector-mediated gene transfer
 and expression in host cell, antibody, agonist, antagonist and DNA
 primer for recombinant vaccine

AUTHOR: Thonnard J
 CORPORATE SOURCE: Rixensart, Belgium.
 PATENT ASSIGNEE: SK-Beecham 2000
 PATENT NUMBER: WO 200047743 PATENT DATE: 20000817 WPI ACCESSION NO.:
 2000-506096 (2045)
 PRIORITY APPLIC. NO.: GB 992937 APPLIC. DATE: 19990210
 NATIONAL APPLIC. NO.: WO 2000EP888 APPLIC. DATE: 20000204
 LANGUAGE: English

ABSTRACT: An *isolated*** *protein*** (164 amino acids) or a *protein*** with at least 85% identity is new. Also claimed are: an immunogenic fragment of the *protein*** with the same activity; a *polynucleotide*** (495 bp) *encoding*** the *protein***; an expression vector; a vaccine composition containing the *protein*** or *polynucleotide*** and a carrier; an antibody; and a therapeutic composition useful in treating *Neisseria*** meningitidis infection. Also disclosed are: a diagnostic kit; *DNA*** primers; screening for agonists or antagonists; agonists and antagonists; modified host cells capable of producing non-live membrane-based bleb vectors; preparation of host cells and bacterial blebs; and computer-based methods for performing homology identification. The *protein*** may be identified within a biological sample from an animal in order to diagnose a N. meningitidis infection. The *Protein*** and *polynucleotide*** may be used for the preparation of a medicament for use in generating an immune response in an animal. The therapeutic composition is useful in a composition for treating humans with N. meningitidis infection. (79pp)

19/3,AB/13 (Item 2 from file: 357)
 DIALOG(R) File 357:Derwent Biotech Res.

09/388090

(c) 2002 Thomson Derwent & ISI. All rts. reserv.

0258602 DBA Accession No.: 2000-13092 PATENT
Neisseria meningitidis BASBO47, BASBO54, BASBO68, and BASBO69 proteins,
useful for treating N. meningitidis infections, bacteremia, and
meningitis - polynucleotide and protein useful for treating disease

AUTHOR: Ruelle J L

CORPORATE SOURCE: Rixensart, Belgium.

PATENT ASSIGNEE: SK-Beecham 2000

PATENT NUMBER: WO 200043519 PATENT DATE: 20000727 WPI ACCESSION NO.:
2000-505839 (2045)

PRIORITY APPLIC. NO.: GB 993535 APPLIC. DATE: 19990216

NATIONAL APPLIC. NO.: WO 2000EP428 APPLIC. DATE: 20000119

LANGUAGE: English

ABSTRACT: A new *isolated*** *protein*** is claimed. It contains an amino
acid sequence which has at least 85% identity to a disclosed residue
*Neisseria*** meningitidis BASBO47, BASBO54, BASBO68, and BASBO69 amino
acid sequence (I-IV). Also claimed are: an *isolated*** *protein***
having any of (I-IV); an *isolated*** *polynucleotide*** containing a
*nucleotide*** sequence *encoding*** a *protein*** that has at least
85% identity to any of (I-IV); an *isolated*** *polynucleotide*** which
contains a *nucleotide*** sequence which has at least 85% identity to
the disclosed bp *DNA*** sequence (V-VIII); an *isolated***
*polynucleotide*** that contains any of (V-VIII); an expression vector
containing an *isolated*** *polynucleotide***; a host cell containing
the expression vector; a process for producing a *protein***; a process
for expressing a *polynucleotide***; a vaccine composition containing
the novel *peptide***; an antibody immunospecific for novel *peptide***
; diagnosing a *Neisseria*** meningitidis infection; and a therapeutic
composition useful in treating *Neisseria*** meningitidis disease. The
*polynucleotide*** and *protein*** can be used in vaccine compositions.
The antibodies can be used in composition for treating *Neisseria***
meningitidis disease. (103pp)

19/3,AB/14 (Item 3 from file: 357)

DIALOG(R)File 357:Derwent Biotech Res.

(c) 2002 Thomson Derwent & ISI. All rts. reserv.

0258174 DBA Accession No.: 2000-12664 PATENT
Antigenic BASB058 polypeptides from Neisseria meningitidis and the nucleic
acids that encode them, useful for vaccinating against bacteria and
meningitis - involving vector-mediated gene transfer for expression in
host cell

AUTHOR: Thonnard J

CORPORATE SOURCE: Rixensart, Belgium.

PATENT ASSIGNEE: SK-Beecham-Biol. 2000

PATENT NUMBER: WO 200044890 PATENT DATE: 20000803 WPI ACCESSION NO.:
2000-491239 (2043)

PRIORITY APPLIC. NO.: GB 992084 APPLIC. DATE: 19990129

NATIONAL APPLIC. NO.: WO 2000EP560 APPLIC. DATE: 20000125

LANGUAGE: English

ABSTRACT: BASB058 antigenic *proteins*** (I) from *Neisseria***
meningitidis and the *nucleic*** acids (II) that *encode*** them, are
claimed. Also claimed are: an *isolated*** *protein*** (I); an
immunogenic fragment of (I); an *isolated*** *polynucleotide*** (II);
an expression vector or recombinant live microorganism; a process for
expressing (II), comprising transforming and culturing a host cell; an

09/388090

antibody specific for (I); and a method of diagnosing a N. meningitidis infection. (I) and (II) may be used according to standard methods to produce vaccine compositions which may be used to vaccinate against (i.e. generate an immune response against) N. meningitidis. The vaccine compositions preferably further contain at least 1 other N. meningitidis antigen. Compositions comprising antibodies specific for (I) may be used to treat N. meningitidis infections in humans. N. meningitidis is implicated in a number of invasive bacterial disease processes such as bacteremia and meningitis. The new *proteins*** and *nucleic*** acids may be used to vaccinate patients against infections which may otherwise be resistant. (75pp)

19/3,AB/15 (Item 4 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2002 Thomson Derwent & ISI. All rts. reserv.

0252760 DBA Accession No.: 2000-07250 PATENT
Neisseria meningitidis NMASP polypeptide, nucleotide sequences and antibodies, useful in vaccines against infection - method is used to induce an immune response to Neisseria meningitidis and Neisseria meningitidis NMASP polypeptide and a NMASP-derived polypeptide in animals

AUTHOR: Jackson W J; Harris A M
CORPORATE SOURCE: Gaithersburg, MD, USA
PATENT ASSIGNEE: Antex-Biologics 2000
PATENT NUMBER: WO 200012535 PATENT DATE: 20000309 WPI ACCESSION NO.:
2000-256581 (2022)
PRIORITY APPLIC. NO.: US 98685 APPLIC. DATE: 19980901
NATIONAL APPLIC. NO.: WO 99US19663 APPLIC. DATE: 19990901
LANGUAGE: English

ABSTRACT: *Neisseria*** meningitidis NMASP *protein*** of mol.wt. 40,000-55,000 (SDS-PAGE) is claimed. Also claimed are: a *peptide*** fragment of NMASP; an *isolated*** antibody that binds NMASP; an antigenic composition (comprises one or more adjuvants) comprising NMASP; an *isolated*** *DNA*** comprising a *nucleotide*** sequence *encoding*** NMASP; an *isolated*** *DNA*** sequence having a 153 base pair sequence; an *isolated*** *DNA*** which comprises a *nucleotide*** sequence that hybridizes to a disclosed sequence; plasmid pNmAH116 obtainable from Escherichia coli; a method (A) for assaying for an agent that interacts with NMASP; an antagonist which inhibits the activity of NMASP; and a method for identifying a compound which interacts with and inhibitor or activate of NMASP. NMASP can be used in a method to produce an immune response in an animal. The sequence and antibody are useful for protection against N. meningitidis, also may be used as ligands to detect antibodies elicited in response to N. meningitidis infection. Antibody generated against the NMASP *polypeptide*** in an animal host will exhibit bactericidal or opsonic activity against many N. meningitidis strains. (75pp)

19/3,AB/16 (Item 5 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2002 Thomson Derwent & ISI. All rts. reserv.

0252684 DBA Accession No.: 2000-07174 PATENT
Non-cytosolic NGSP polypeptide and polynucleotide sequence from Neisseria useful for diagnosis, prevention or treatment of Neisseria infections

Searcher : Shears 308-4994

09/388090

- method is used for inducing an immune response to Neisseria and Neisseria
NGSP polypeptide and a NGSP-derived polypeptide in animal

AUTHOR: Jackson W J; Harris A M

CORPORATE SOURCE: Gaithersburg, MD, USA.

PATENT ASSIGNEE: Antex-Biologics 2000

PATENT NUMBER: WO 200012133 PATENT DATE: 20000309 WPI ACCESSION NO.:

2000-237782 (2020)

PRIORITY APPLIC. NO.: US 98685 APPLIC. DATE: 19980901

NATIONAL APPLIC. NO.: WO 99US20070 APPLIC. DATE: 19990901

LANGUAGE: English

ABSTRACT: *Isolated*** NGSP *protein*** (I) of *Neisseria*** spp. having a
mol.wt. of 40,000-55,000 (from *Neisseria*** *ovis***, *Neisseria***
*osloensis***, *Neisseria*** *bovis***, *Neisseria*** *gonorrhoeae***
or *Neisseria*** *lacunata***) is claimed. (I) is a subunit of a
non-cytosolic *protein*** located in the bacterial envelope. Also
claimed are: a *peptide*** fragment (II) of (I); an antibody (III) that
binds (I); an antigenic composition containing (I) or (II); a
pharmaceutical composition of (III); an *isolated*** *DNA*** (IV)
comprising a *nucleotide*** sequence *encoding*** (I) or (II); an
*isolated*** *DNA*** comprising a sequence which hybridizes to (IV);
plasmid pTLZ-NgHtrA number 2 from Escherichia coli JM109; a
(I)-antagonist which inhibits (I) activity; a method for identifying
compounds which inhibit (I) activity to permit interaction between (A)
and (I); and a method for assaying for an agent that interacts with (I)
which involves washing the cells and detecting any marker associated
with the cells. (I) and (II) can be used to immunize an animal, and
also as a ligand to detect antibodies elicited in response to
*Neisseria*** infections or as an antigen to induce *Neisseria***
-specific antibodies. (68pp)

19/3,AB/17 (Item 6 from file: 357)

DIALOG(R)File 357:Derwent Biotech Res.

(c) 2002 Thomson Derwent & ISI. All rts. reserv.

0248452 DBA Accession No.: 2000-02942 PATENT

New polypeptide from Neisseria meningitidis useful for diagnosis, treatment
or prevention of bacterial infections in mammal - diagnosis,
prophylaxis, therapy, gene therapy, recombinant vaccine and nucleic
acid vaccine

AUTHOR: Ruelle J L

CORPORATE SOURCE: Rixensart, Belgium.

PATENT ASSIGNEE: SK-Beecham-Biol. 1999

PATENT NUMBER: WO 9958683 PATENT DATE: 19991118 WPI ACCESSION NO.:

2000-053103 (2004)

PRIORITY APPLIC. NO.: GB 9810276 APPLIC. DATE: 19980513

NATIONAL APPLIC. NO.: WO 99EP3255 APPLIC. DATE: 19990507

LANGUAGE: English

ABSTRACT: An *isolated*** *protein*** (I), BASB029 from *Neisseria***
meningitidis comprises 594 and 591 amino acids (*protein*** sequences
disclosed). Also claimed are: a *protein*** 85% or 95% identical to
(I); an immunogenic fragment of (I) with the same immunogenic activity
as (I); an *isolated*** *polynucleotide*** (II) *encoding*** (I) and
having a sequence of 1,785 and 1,776 bp; a *polynucleotide*** (III)
having a sequence complementary to (II); a *polynucleotide*** (IV) 85%
identical to (II) or its complement; an expression vector or
recombinant live microorganism comprising (II), (III) or (IV); a host
cell containing the vector or a subcellular fraction of a membrane of a

09/388090

host cell expressing (I); producing (I) by culturing the transformed host cell under conditions and recovering (I) from the culture medium; expressing (II), (III) or (IV) by transforming host cells and growing them under conditions suited to expression; a recombinant vaccine containing (I); a *nucleic*** acid vaccine containing (II), (III) or (IV); and an antibody immunospecific for (I) or the immunological fragment. (74pp)

? log y

17jun02 10:22:48 User219783 Session D1832.2